

Figure 1

1 GGCACGAGGTGCACAGGAAGGATGAGGAAGACCAGGCTCTGGGGGCTGCTGTGGATGCTC 60
1 M R K T R L W G L L W M L 13

61 TTTGTCTCAGAACTCCGAGCTGCAACTAAATTAAGTGAAGAAAAGTATGAAGTGAAGAG 120
14 F V S E L R A A T K L T E E K Y E L K E 33

121 GGGCAGACCCCTGGATGTGAAATGTGACTACACGCTAGAGAAGTTTGCCAGCAGCCAGAAA 180
34 G Q T L D V K C D Y T L E K F A S S Q K 53

181 GCTTGGCAGATAATAAGGGACGGAGAGATGCCCAAGACCCCTGGCATGCACAGAGAGGCT 240
54 A W Q I I R D G E M P K T L A C T E R P 73

241 TCAAAGAATTCCCATCCCAATGCCAAGTGGGGAGGATCATACTAGAAGACTACCATGATCAT 300
74 S K N S H P V Q V G R I I L E D Y H D H 93

301 GGTTTACTGCGCTCCGAATGGTCAACCTTCAAGTGAAGATTCTGGACTGTATCAGTGT 360
94 G L L R V R M V N L Q V E D S G L Y Q C 113

361 GTGATCTACAGCCCTCCCAAGGAGGCTCAGATGCTGTTCGATCGCATCCGCTTGGTGGT 420
114 V I Y Q P P K E P H M L F D R I R L V V 133

421 ACCAAGGGTTTTTCAGGGACCCCTGGCTCCAATGAGAATTCTACCCAGATGTGTATAAG 480
134 T K G F S G T P G S N E N S T Q N V Y K 153

481 ATTCTCTTACCACCACTAAGGCCTTGTGCCCACTCTATACCAGCCCAAGTGTGACC 540
154 I P P T T T K A L C P L Y T S P R T V T 173

541 CAAGCTCCACCAAGTCAACTGCCGATGTCTCCACTCTGACTCTGAAATCAACCTTACA 600
174 Q A P P K S T A D V S T P D S E I N L T 193

601 AATGTGACAGATATCATCAGGGTTCGGGTGTTCAACATTGTCACTTCTCCTGGCTGGTGA 660
194 N V T D I I R V P V F N I V I L L A G G 213

661 TTCCTGAGTAAGAGCCTGGTCTCTCTGTCTGCTGTTTGTCTGTCAGCGTGAGGTCAATTGTA 720
214 F L S K S L V F S V L F A V T L R S F V 233

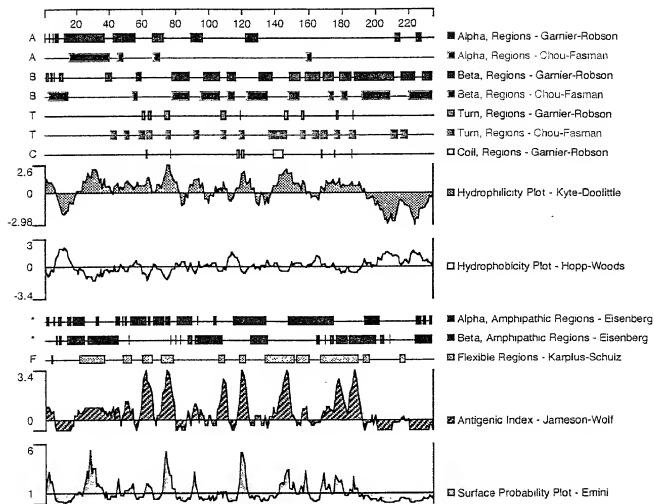
721 CCCTAGGCCCACGAACCCACGAGAATGTCCTCTGACTTCCAGCCACATCCATCTGGCAGT 780
234 P * 235

781 TGTGCCAAGGGAGGGAGGAGGTTAAAGGCAGGGAGTTAATAACATGAATTAAATCTG 840

841 TAATCACCAGCTAAAAAAAAAAAAAAAAAAAA 870

09662771.061801

Figure 2



0000271.051804